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?ds
Set     Items   Description
S1          4   POINSETTIA AND AFLP
S2          3   RD (unique items)
S3          2   FINGERPRINT(S)POINSETTIA
S4          2   RD (unique items)
S5          7   GENOTYPE(S)POINSETTIA
S6          4   RD (unique items)
S7         16   EUPHORBIA(W)CYATHOPHORA
S8        159   EUPHORBIA(S)(CULTIVAR OR BREEDING(W)FAMILY)
S9          0   S7 AND AFLP
S10         1   S8 AND AFLP
S11     11775   EUPHORBIA
S12         7   S11 AND AFLP
S13         5   RD (unique items)
S14      1815   (SNP OR POLYMORPHI? OR VARIANT OR MUTANT OR AFLP) AND (DICE
               OR JACCARD OR LYNCH OR SIMILARITY(N)INDEX OR DISSIMILARITY(N-
               )INDEX)
S15         1   PROFILE(W)INDEX(W)VALUE
S16         1   S15 AND S14
S17      2639   SIMILARITY(N)INDEX OR DISSIMILARITY(N)INDEX
S18       477   S17 AND (CULTIVAR OR PLANT)
S19       137   S18 AND (DAF OR RFLP OR AFLP OR RAPD OR AP(W)PCR OR SSR OR
               ASAP)
S20        75   RD (unique items)
S21        39   S20 NOT PY>2000
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Dialog (Biotech)
2/24/04

Sinclair in West

24/3,AB/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012546591 BIOSIS NO.: 200000264904
Identification of species and varieties in Brassica plants as oil crops by RAPD
AUTHOR: Tanaka Shigeo (Reprint); Ma Jinxia (Reprint); Matsushita Keisuke (Reprint); Futsuhara Yuzo (Reprint)
AUTHOR ADDRESS: Faculty of Agriculture, Meijo University, Tempaku, Nagoya, 468-8502, Japan**Japan
JOURNAL: Scientific Reports of the Faculty of Agriculture Meijo University (36): p39-45 March, 2000 2000
MEDIUM: print
ISSN: 0910-3376
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Japanese

ABSTRACT: Genomic DNAs are extracted from 11 varieties belonging to Brassica campestris L., two varieties to B. napus L., and two varieties to B. juncea (L.) Czern, developed in Xinjiang, China as oil crops. Their DNAs were analyzed by **RAPD** using PCR with 16 kinds of 10-mer primers for probes. The original bands in each species were detectable in primers S17 and Y18. Dendrograms were depicted from **similarity index**, genetical distance, correlation coefficient and Euclid distance in principal component analysis. These three species could genealogically be discriminated by comparing **similarity index**, genetical distance and correlation coefficient in primer S17 and **similarity index** and genetical distance in primer Y18. Compared to the previous reports, authors could find much more bands. Species with genome A was closely correlated with ones with genome B. The main reason for the success of identification in the different three species might be ascribed to many-sided approaches such as **RAPD**, PCA, dendrogram and image analyses. In particular, it was proved that the DNA polymorphisms would be useful for discriminating the genealogical relationships among the different species and varieties.

24/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012403920 BIOSIS NO.: 200000122233
Randomly amplified polymorphic DNA analysis of Vitis species and Florida bunch grapes
AUTHOR: Wang Y; Chen J; Lu J; Lamikanra O (Reprint)
AUTHOR ADDRESS: Southern Regional Research Center, United States Department of Agriculture, 1100 Robert E. Lee Boulevard, New Orleans, LA, 70124, USA **USA
JOURNAL: Scientia Horticulturae (Amsterdam) 82 (1-2): p85-94 Dec. 1, 1999 1999
MEDIUM: print
ISSN: 0304-4238
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Randomly amplified polymorphic DNA (**RAPD**) analysis was performed on 42 accessions of Vitis, representing 13 species. Inter- and intra-specific/varietal variation were observed. Principal component analysis of Nei and Li's **similarity index** separated V. rotundifolia from other bunch-grape species. Within the bunch-grape species, V. vinifera, the North American bunch grapes, and the East Asian bunch grapes formed three separate **RAPD** clusters. **RAPD** analysis also demonstrated its sensitivity by detecting the genetic diversity within Florida bunch-grape cultivars. **RAPD** analysis, together with the published morphological data, will lead to a more comprehensive understanding of Vitis genetic diversity.

24/3,AB/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012246352 BIOSIS NO.: 199900506012
Use of molecular markers for diversity analysis in rice
AUTHOR: Nadarajan N (Reprint); Vivekanandan P; Henry Robert J
AUTHOR ADDRESS: Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, 625 104, India**India
JOURNAL: Indian Journal of Genetics and Plant Breeding 59 (3): p247-259 Aug., 1999 1999
MEDIUM: print
ISSN: 0019-5200
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The genetic relationship between seven japonica, two indica and one tropical japonica rice varieties was analysed by using PCR with Random Amplified Polymorphic DNA (**RAPD**) and Amplified Fragment Length Polymorphism (**AFLP**) methods. In **RAPD** analysis PCR with 10 arbitrary primers applied to ten rice varieties produced 84 useful markers, of which 77.4% were polymorphic. Fifteen **AFLP** primer combinations produced 285 markers, of which 70.8% were polymorphic. Thus, sufficient polymorphism could be detected to allow identification of individual varieties. Visual examination of electrophoresis gels and analysis of banding patterns confirmed that all the seven japonica types were closely related, with similarity indices of 50-85%. Two indica varieties were classified into separate group. However, the tropical japonica type was easily distinguished, producing variety specific amplification profiles and expressing a lower **similarity index** to all other varieties tested. Thus, both **RAPD** and **AFLP** methods offer a potentially simple, rapid and reliable method for rice genotype identification and recognition of lines that could contribute genetic diversity to new commercial varieties. **AFLP** was more useful than **RAPD** because the potential number of loci that could be assayed with **AFLP** far exceeds that with **RAPD** .

24/3,AB/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012196258 BIOSIS NO.: 199900455918
Low-Cot DNA sequences for fingerprinting analysis of germplasm diversity and relationships in Amaranthus
AUTHOR: Sun M (Reprint); Chen H; Leung F C
AUTHOR ADDRESS: Department of Zoology, University of Hong Kong, Pokfulam Road, Hong Kong, China**China
JOURNAL: Theoretical and Applied Genetics 99 (3-4): p464-472 Aug., 1999 1999
MEDIUM: print
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We examined genetic diversity and relationships among 24 cultivated and wild Amaranthus accessions using the total low-Cot DNA and five individual repetitive sequences as probes. These low-Cot DNA probes were obtained by the isolation of various classes of repetitive-DNA sequences, including satellites, mini-satellites, microsatellites, rDNA, retrotransposon-like sequences, and other unidentified novel repetitive sequences. DNA fingerprints generated by different types of repetitive-DNA probes revealed different levels of polymorphism in the Amaranthus genomes. A repetitive sequence containing microsatellites was found to be a suitable probe for characterizing intraspecific accessions,

whereas more conservative sequences (e.g. rDNA) were informative for resolving phylogenetic relationships among distantly related species. Genetic diversity, measured as restriction fragment length polymorphism (**RFLP**) and the **similarity index** at the low-Cot DNA level, was equally high among intraspecific accessions between the two species groups: grain amaranths (A. caudatus, A. cruentus, and A. hypochondriacus) and their putative wild progenitors (A. hybridus, A. powellii, and A. quitensis). At the interspecific level, however, the grain amaranth species are less divergent from each other than their wild progenitors. With the rare exceptions of certain A. caudatus accessions, grain amaranths were found to be closely related to A. hybridus. The results based on low-Cot DNA were comparable with previous **RAPD** and isozyme studies of the same set of species/accessions of Amaranthus, indicating that low-Cot DNA sequences are suitable probes for a fingerprinting analysis of **plant** germplasm diversity and for determining phylogenetic relationships.

24/3,AB/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012059708 BIOSIS NO.: 199900319368
Random primed polymerase chain reaction differentiates Codonopsis pilosula from different localities
AUTHOR: Zhang Yan-Bo; Ngan Fai-Ngor; Wang Zheng-Tao; Ng Tzi-Bun; But Paul Pui-Hay; Shaw Pang-Chui; Wang Jun (Reprint)
AUTHOR ADDRESS: Department of Biochemistry, Chinese University of Hong Kong, Shatin, New Territories, Hongkong, China**China
JOURNAL: Planta Medica 65 (2): p157-160 March, 1999 1999
MEDIUM: print
ISSN: 0032-0943
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: DNA fingerprints distinctive among the samples from different localities in China were successfully reproduced for the Chinese herb Dangshen, the roots of Codonopsis pilosula, (Campanulaceae). **Similarity index** (S.I.) analysis revealed that C. pilosula samples from the same province generated similar DNA fingerprints, while samples of different provinces displayed different DNA fingerprints. This method may be a general and valuable tool for locality authentication of other Chinese herbal medicinal materials.

24/3,AB/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011647842 BIOSIS NO.: 199800442089
Hybrid performance and genetic distance as revealed by the (GATA)4 microsatellite and RAPD **markers in pearl millet**
AUTHOR: Chowdari K V; Venkatachalam S R; Davierwala A P; Gupta V S; Ranjekar P K (Reprint); Govila O P
AUTHOR ADDRESS: Plant Mol. Biol. Unit, Div. Biochem. Sci., Natl. Chem. Lab., Pune 411008, India**India
JOURNAL: Theoretical and Applied Genetics 97 (1-2): p163-169 July, 1998 1998
MEDIUM: print
ISSN: 0040-5752
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Genetic diversity in five cytoplasmic male-sterile and seven restorer lines of pearl millet was determined by DNA fingerprinting using a (GATA)4 microsatellite and randomly amplified polymorphic DNAs (RAPDs). A total of 160 polymorphic loci were generated and, based on the polymorphism data, **similarity index** values ranged from 0.81 to 0.50.

Cluster analysis was performed and relationships among these lines revealed that they were not in agreement with the available pedigree data. The per se performance of parents and hybrids was analyzed for days-to-50% flowering, **plant** height, productive tillers, ear length, ear width, 1000-grain weight and grain yield per plot. Path co-efficient analysis revealed that productive tillers, ear width and days-to-50% flowering had a relatively large positive effect. The correlation values were mostly not significant with respect to genetic distance, except for days-to-50% flowering, ear length and ear width. Our results have indicated that genetic-distance measures based on the (GATA)4 microsatellite and RAPDs may be useful for the grouping of parents, but not for predicting heterotic combinations, in pearl millet.

24/3,AB/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011647790 BIOSIS NO.: 199800442037
Assessment of genetic variation in a working collection of Vigna vexillata (L.) A. Rich. by isozyme and RAPD **analyses**
AUTHOR: Spinosa Anne; Pignone Domenico; Sonnante Gabriella (Reprint)
AUTHOR ADDRESS: CNR-Ist. Germoplasma, Via Amendola 165/A, 70126 Bari, Italy **Italy
JOURNAL: Genetic Resources and Crop Evolution 45 (4): p347-354 Aug., 1998 1998
MEDIUM: print
ISSN: 0925-9864
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Genetic variation based on isozyme and **RAPD** analyses was investigated in 47 and 34 accessions respectively of Vigna vexillata from different geographical origins and belonging to three botanical varieties. A total of 9 enzyme systems were studied, accounting for 14 putative loci, 8 of which were polymorphic. The analysis of genetic diversity revealed a low level of within accession variation (HS = 0.013), while between accession diversity (DST) was 0.120. Coefficient of gene differentiation (GST) was 0.905, indicating that most variation was among accessions. Nei's genetic distances were calculated on the basis of allelic frequencies and a UPGMA dendrogram was constructed. Twenty arbitrary 10-mer oligonucleotides were used in **RAPD** analysis. Amplification profiles disclosed a higher level of polymorphism than isozymes. Based on amplification patterns, the **similarity index** of Jaccard was calculated and a dendrogram constructed on the basis of the similarity matrix. The final clustering based on **RAPD** data was similar to the one obtained using isozyme allelic frequencies. The classification in botanical varieties did not reflect the allelic constitution of the different samples. On the other hand, referring to geographical origin, most accessions from Africa and from Latin America were distributed respectively in two distinct clusters in the dendrogram. This grouping might also reflect the differences observed in the germination behaviour of V. vexillata from the two continents.

24/3,AB/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011605646 BIOSIS NO.: 199800399893
Genetic diversity analysis of Oryza using amplified fragment length polymorphism
AUTHOR: Singh Sukhwinder; Sidhu J S; Uberoi S K; Sodhi M; Vikal Y; Dhaliwal H S
AUTHOR ADDRESS: Biotechnol. Centre, Punjab Agric. Univ., Ludhiana, 141 004 Punjab, India**India
JOURNAL: Crop Improvement 25 (1): p15-20 June, 1998 1998
MEDIUM: print

ISSN: 0256-0933
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Amplified Fragment Length Polymorphism (**AFLP**) analysis was carried out to study the genetic diversity among eight cultivars of Oryza saliva L. and seven accessions of four wild Oryza species. UPGMA analysis of 130 **AFLP** loci visualized among Oryza lines was performed. At 60 per cent **similarity index** , all the cultivars grouped into one cluster, all the accessions of A genome into another group, whereas the only accession of O. brachyantha (FF) and O. punctata (BBCC) remained isolated. However, at 80 per cent **similarity index** , all cultivars grouped into one cluster **AFLP** markers were able to efficiently discriminate various cultivars and species of Oryza.

24/3,AB/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011462886 BIOSIS NO.: 199800257133
Genetic characterization and relatedness among California almond cultivars and breeding lines detected by randomly amplified polymorphic DNA (RAPD) analysis
AUTHOR: Bartolozzi F (Reprint); Warburton M L; Arulsekar S; Gradziel T M
AUTHOR ADDRESS: C.N.R. Inst. Ricerche Olivicoltura, 05128 Perugia, Italy** Italy
JOURNAL: Journal of the American Society for Horticultural Science 1223 (3): p381-387 May, 1998 1998
MEDIUM: print
ISSN: 0003-1062
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Almond (Prunus dulcis (Mill.) D.A. Webb, syn. P. amygdalus, Batsch; P. communis (l.) Archangeli) represents a morphologically and physiologically variable group of populations that evolved primarily in central and southwest Asia. California cultivars have been developed from highly selected subgroups of these populations, while new breeding lines have incorporated germplasm from wild almond and closely related peach species. The genetic relatedness among 17 almond genotypes and 1 peach genotype was estimated using 37 **RAPD** markers. Genetic diversity within almond was found to be limited despite its need for obligate outcrossing. Three groupings of **cultivar** origins could be distinguished by **RAPD** analysis: bud-sport mutations, progeny from interbreeding of early California genotypes, and progeny from crosses to genotypes outside the California germplasm. A **similarity index** based on the proportion of shared fragments showed relatively high levels of 0.75 or greater within the almond germplasm. The level of similarity between almond and the peach was 0.424 supporting the value of peach germplasm to future almond genetic improvement.

24/3,AB/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011346847 BIOSIS NO.: 199800141094
Isozyme and RAPD **polymorphisms in Heterobasidion annosum in Italy**
AUTHOR: Goggioli V (Reprint); Carpetti P; Hamelin R C; Vendramin G G
AUTHOR ADDRESS: Ist. Patol. Zool. Forestale Agraria, Univ. Firenze Piazzale delle Cascine, 28, I-50144 Firenze, Italy**Italy
JOURNAL: European Journal of Forest Pathology 28 (1): p63-74 Jan., 1998 1998
MEDIUM: print
ISSN: 0300-1237
DOCUMENT TYPE: Article

RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Isozyme and random amplified polymorphic DNA (**RAPD**) polymorphisms were used to study variability in a group of 41 isolates from the Italian population of Heterobasidion annosnum. The isolates belonged to the intersterility groups P and S, and particularly to the group that is most widely distributed in Italy, group F. Isozyme analysis was effective in identifying the three intersterility groups and revealed a high degree of genetic divergence within the P group isolates; the mannose phosphate isomerase (MPI-2) locus was diagnostic in the attribution of isolates to the more correlated F and S groups. RAPDs were detected following amplification by the polymerase chain reaction (PCR). 74 **RAPD** fragments, obtained through amplifications with eight primers, were scored. Isolates from the 3 intersterility groups were clearly divergent based on analysis of **RAPD** markers. However, a **similarity index** calculated for the isolates within the F population indicated a high uniformity of the isolates collected throughout the Italian peninsula.

24/3,AB/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011320937 BIOSIS NO.: 199800115184
Phylogenetic relationships of industrial chicory varieties revealed by RAPDs and AFLPs
AUTHOR: Koch G (Reprint); Jung C
AUTHOR ADDRESS: Inst. Pflanzenbau und Pflanzenzuechtung, Christian-Albrechts-Univ. Kiel, Olshausenstr. 40, 24118 Kiel, Germany** Germany
JOURNAL: Agronomie (Paris) 17 (6-7): p323-333 July-Sept., 1997 1997
MEDIUM: print
ISSN: 0249-5627
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Seventeen industrial chicory varieties were subjected to molecular marker analysis revealing genetic variation within varieties and genetic relationships between varieties. Banding profiles from 66 **RAPD** loci (random amplified polymorphic DNA) and 171 **AFLP** loci (amplified fragment length polymorphism) were produced with total genomic chicory DNA of leaf bulks from four to eight plants per variety. The DICE **similarity index** was calculated and transformed to genetic distances for construction of phylogenetic trees. We found that there was no clear and strict grouping of the varieties. Genetics distances were nearly the same between all varieties. Marker analysis of individual plants of the variety Fredonia revealed a considerable degree of intravarietal typical for open pollinated varieties. The following conclusions was drawn: 1) among the root chicory varieties distant phylogenetic groups do not exist or formerly existing groups were eroded by successive intercrosses; 2) potentially existing phylogenetic or heterotic group structures are concealed by the high within population genetic variability; 3) the selection/breeding intensities were low during the last decades; and (4) the high degree of genetic variability can be used for selecting superior genotypes from already existing varieties by mass selection.

24/3,AB/12 (Item 12 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011166528 BIOSIS NO.: 199799800588
Application of RAPD fingerprinting in selection of micropropagated plants of Piper longum for conservation
AUTHOR: Parani M; Anand Ajith; Parida Ajay
AUTHOR ADDRESS: M. S. Swaminathan Res. Foundation, III Cross Road, Taramani

Institutional Area, Madras 600 013, India**India
JOURNAL: Current Science (Bangalore) 73 (1): p81-83 1997 1997
ISSN: 0011-3891
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Random amplified polymorphic DNA fingerprints of twenty micropropagated plants and the mother **plant** were analysed by polymerase chain reaction of genomic DNA using ten random 10-mer primers. The **RAPD** fragments were scored for presence/absence to calculate Jaccard's **similarity index** . Clustering based on **similarity index** was done following unweighted pair group with arithmetic mean method and a dendrogram was constructed. The dendrogram showed eighteen micropropagated plants forming a major cluster along with the mother **plant** . The other two micropropagated plants could be regarded as molecular off-types (putative somaclonal variants) as they have shown less than 80% similarity to the mother **plant** and other micropropagated plants. Among the eighteen micropropagated plants of the major cluster the order of preference to maintain maximum fidelity to the elite genotype (the mother **plant**) for conservation was established.

24/3,AB/13 (Item 13 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0011073196 BIOSIS NO.: 199799707256
RAPD **and morphological analysis of the rare** plant **species Vicia pisiformis (Fabaceae)**
AUTHOR: Black-Samuelsson Sanna (Reprint); Eriksson Gosta; Gustafsson Lena; Gustafsson Petter
AUTHOR ADDRESS: Dep. Forest Genetics, Swedish Univ. Agric. Sci., P.O. Box 7027, S-750 07 Uppsala, Sweden**Sweden
JOURNAL: Biological Journal of the Linnean Society 61 (3): p325-343 1997 1997
ISSN: 0024-4066
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The amount and pattern of genetic variation was surveyed in two Swedish and three Czech populations of the rare perennial forest **plant** Vicia pisiformis. This species has a mainly easterly-continental European distribution and has few and small populations in Sweden. It is classified as 'vulnerable' on the Swedish Red Data list. Seeds from natural populations were collected and grown under controlled conditions in growth chambers. The variation was estimated in growth and fecundity traits and with Random Amplified polymorphic DNA, **RAPD** . Low inter- and intra-population variation in **RAPD** -markers was found using 11 primers, with a **similarity index** (Wetton) for the families of 0.98. In contrast, multivariate analysis of variance showed significant morphological differences within and between populations. Also in the univariate ANOVAs, a number of the traits showed significant between- and/or within population differentiation. Cluster analysis for the morphological traits and RAPDs (UPGMA) did not structure the variation of families in accordance with their geographical distance. A Mantel test based on comparisons between Mahalonobis and Jaccard distance for morphological and **RAPD** data, respectively, did not reveal any significant correlation between the two matrices. It is concluded that if a genetic conservation program is to be applied on Vicia pisiformis, different sampling strategies are needed to capture morphological vs **RAPD** variation. This is, to our knowledge, the first investigation that compares **RAPD** and morphological variation in a threatened **plant** species.

24/3,AB/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010546071 BIOSIS NO.: 199699180131
Comparative studies on the Hanabusaya asiatica and its allied groups based on randomly amplified polymorphic DNA (RAPD) analysis
AUTHOR: Yoo Ki Oug; Lee Woo Tchul; Kim Nam Soo; Kim Jong Hwa; Lim Hak Tae (Reprint)
AUTHOR ADDRESS: Dep. Hortic., Kangwon Natl. Univ., Chunchon 200-701, South Korea**South Korea
JOURNAL: Journal of the Korean Society for Horticultural Science 37 (2): p 324-328 1996 1996
ISSN: 0253-6498
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: Korean

ABSTRACT: The phylogenetic relationships between Korean endemic Hanabusaya asiatica, and its allied groups including four genera and nine species were investigated at the DNA level using Randomly Amplified Polymorphic DNA (**RAPD**) method. Ten primers out of 80 primers (10-mer) screened gave rise to very high polymorphism (99%) in all of the tested plants, producing 153 randomly amplified DNA fragments. H. asiatica was differentiated from its allied groups at the 0.62 of **similarity index** of RAPDs. This results were in accordance with previous classification based on morphological studies. It was confirmed that H. asiatica could be placed into Korean endemic and suggested that **RAPD** technique be used as an additional method of phylogenetic relationship for **plant** systematics.

24/3,AB/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010517974 BIOSIS NO.: 199699152034
Extent of RFLP **variability in tetraploid populations of alfalfa, Medicago sativa**
AUTHOR: Pupilli F (Reprint); Businelli S (Reprint); Paolocci F (Reprint); Scotti C; Damiani F (Reprint); Arcioni S (Reprint)
AUTHOR ADDRESS: Ist. Ricerche sul Miglioramento Genetico, Piante Foraggere CNR, Via Madonna 130, I-06128 Perugia, Italy**Italy
JOURNAL: Plant Breeding 115 (2): p106-112 1996 1996
ISSN: 0179-9541
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Seven widely-cultivated alfalfa varieties and three ecotypes adapted to Central Italy were used to evaluate the extent of polymorphism in that species. Twenty plants per accession were analysed with 16 **RFLP** probes combined with three restriction enzymes (48 probe/enzyme combination in total) and the data were used to compute the Nei's **similarity index** taken as a measure of inter- and intra-population **RFLP** variability. The varieties were, in general, more homogeneous than the ecotypes and the cultivars 'Adriana' and 'Florida' could be differentiated more easily than the others. Few accession-specific hybridizing fragments were scored and seven populations could be distinguished from the others on the basis of significant differences in the frequencies of specific fragments. The DNA of **plant** populations of several sizes was bulked and the ability to detect a given fragment in pooled samples was related to the fraction of plants having that fragment among the plants forming the bulk. The results are discussed with special emphasis on the practical utilization of RFLPs for varietal identification.

24/3,AB/16 (Item 16 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010453502 BIOSIS NO.: 199699087562
Genetic similarities among wine grape cultivars revealed by restriction fragment-length polymorphism (RFLP) analysis
AUTHOR: Bowers John E; Meredith Carole P
AUTHOR ADDRESS: Dep. Viticulture Enol., Univ. California, Davis, CA 95616, USA**USA
JOURNAL: Journal of the American Society for Horticultural Science 121 (4): p620-624 1996 1996
ISSN: 0003-1062
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: **RFLP** data were used to assess genetic similarity among 33 Vitis vinifera L. cultivars and one interspecific **cultivar** . A similarity matrix was constructed on the basis of the presence or absence of 49 bands generated by eight **RFLP** probes and cluster analysis was performed. The mean **similarity index** for all pairwise comparisons was 0.696 and ranged from 0.444 between 'St. Emilion' and the interspecific hybrid 'Salvador' to 0.952 between 'Chenin blanc' and 'Semillon'. Mean similarity among all V. vinifera cultivars was 0.705. Several groupings of similar cultivars are consistent with historical reports and presumed geographic origins: 'Chardonnay' and 'Melon', 'Colombard' and 'Folle blanche', 'Gewurztraminer' and 'Trousseau', 'Cabernet franc' and 'Cabernet Sauvignon', 'Mission' and 'Palomino'. The similarity between 'Mission, and 'Palomino' is the first genetic evidence to support the putative Spanish origin of 'Mission'. Some groupings are unexpected ('Sauvignon blanc' and 'Gewurztraminer', 'Chenin blanc' and 'Semillon') because the cultivars are not thought to have originated in the same regions. While some relationships suggested by this study may be artifacts of **RFLP** analysis or of the statistical method, they raise questions for further genetic inquiry into the origins of grape cultivars.

24/3,AB/17 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010323843 BIOSIS NO.: 199698791676
Genetic variation among and within United States collard cultivars and landraces as determined by randomly amplified polymorphic DNA markers
AUTHOR: Farnham Mark W
AUTHOR ADDRESS: U.S. Dep. Agric., Agric. Research Serv., U.S. Vegetable Lab., 2875 Savannah Highway, Charleston, SC 29414-5334, USA**USA
JOURNAL: Journal of the American Society for Horticultural Science 121 (3): p374-379 1996 1996
ISSN: 0003-1062
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A collection of collard (Brassica oleracea L., Acephala group) germplasm, including 13 cultivars or breeding lines and 5 landraces, was evaluated using randomly amplified polymorphic DNA (**RAPD**) markers and compared to representatives of kale (Acephala group), cabbage (Capitata group), broccoli (Italica group), Brussels sprouts (Gemmifera group), and cauliflower (Botrytis group). Objectives were to assess genetic variation and relationships among collard and other crop entries, evaluate intrapopulation variation of open-pollinated (OP) collard lines, and determine the potential of collard landraces to provide new B. oleracea genes. Two hundred nine **RAPD** bands were scored from 18 oligonucleotide decamer primers when collard and other B. oleracea entries were compared. Of these, 147 (70%) were polymorphic and 29 were specific to collard. Similarity indices between collard entries were computed from **RAPD** data and these ranged from 0.75 to 0.99 with an average of 0.83. Collard entries were most closely related to cabbage (**similarity index** = 0.83) and Brussels sprouts entries (index = 0.80). Analysis of

individuals of an OP **cultivar** and landrace indicated that intrapopulation genetic variance accounts for as much variation as that observed between populations. **RAPD** analysis identified collard landraces as unique genotypes and showed them to be sources of unique DNA markers. The systematic collection of collard landraces should enhance diversity of the B. oleracea germplasm pool and provide genes for future crop improvement.

24/3,AB/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009813641 BIOSIS NO.: 199598281474
Classification of Mume (Prunus mume Sieb. et Zucc.) by RAPD **Assay**
AUTHOR: Shimada Takehiko (Reprint); Haji Takashi; Yamaguchi Masami; Takeda Toshihide (Reprint); Nomura Keiichi (Reprint); Yoshida Masao (Reprint)
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JOURNAL: Journal of the Japanese Society for Horticultural Science 63 (3): p543-551 1994 1994
ISSN: 0013-7626
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The genetic relationship of mume cultivars was resolved by random amplified polymorphic DNA (**RAPD**) assay using 95 decamer oligonucleotide primers. The heterozygosity within Prunus mume was confirmed by the numerous polymorphism of DNA fingerprints which exist among cultivars. Representative cultivars were selected from four groups; 1) Ko-ume (small fruit), 2) Chuu-ume (medium fruit), 3) Ou-ume (large fruit), 4) hybrid between mume and apricot; which were generally classified by fruit size and morphological traits. Japanese mume **cultivar** were developed independently as indicated by the **dissimilarity index** between Taiwan and Japanese mume. The Ko-ume and Taiwan mume group with its narrow genetic variation are different from 'Bungo' which has characteristics of the apricot. Thus, they are genetically distant from 'Bungo' and apricot. Four flowering mume cultivars in this experiment are closely related to the fruiting mume but were classified into a segregate group, because a possibility exists that the fruiting mume may be a derivative of the flowering ones. The 3 groups of mume cultivars: 1) 'Muroya', 'Inazumi', and 'Tounoume'; 2) 'Komukai' and 'Gojirou'; and 3) 'Suzukishiro' and 'Taihei' consists of synonyms. Therefore, they could not be distinguished from each other with precise **RAPD** assay capable of detecting DNA polymorphisms. The possibility seems to be high that the cultivars within the 3 groups are identical. 'Takadaume' was shown as the nearest to apricot among mume cultivars. 'AM2-1', 'AM2-2' and 'AM2-4' which are artificial hybrids between 'Jizouume' and 'Heiwa' were classified into the same cluster as 'Bungo'. It is sufficient evidence to prove that 'Bungo' is a hybrid between mume and apricot. It seems reasonable to suppose that **RAPD** assay has the potentiality to identify mume cultivars, considering the capability of discriminating these artificial hybrids. In conclusion, mume cultivars can be classified into seven groups: 1) Taiwan mume, 2) Ko-ume (small fruit), 3) Chuu-ume (medium fruit), 4) Ou-ume (large fruit) with white flower, 5) Ou-ume (large fruit) with pink flower, 6) Anzu-ume or Bungo-ume (apricot-mume hybrid), 7) Sumomo-ume (plum-mume hybrid). The DNA fingerprints of mume genome generated by **RAPD** assay reflect the own origin of mume cultivars. Hence, the method is expected to contribute to a mume breeding project.

24/3,AB/19 (Item 19 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0009664629 BIOSIS NO.: 199598132462
Random amplified polymorphic DNA analysis of Australian rice (Oryza sativa L.) varieties
AUTHOR: Ko H L (Reprint); Cowan D C (Reprint); Henry R J (Reprint); Graham

G C (Reprint); Blakeney A B; Lewin L G
AUTHOR ADDRESS: Queensland Dep. Primary Industries, Queensland Agric. Biotechnol. Cent., Gehrmann Lab., Univ. Queensland, QLD 4072, Australia** Australia
JOURNAL: Euphytica 80 (3): p179-189 1994 1994
ISSN: 0014-2336
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The genetic relationships between rice varieties were analysed by using the polymerase chain reaction (PCR), with arbitrary oligonucleotide primers in the random amplified polymorphic DNA (**RAPD**) method. PCR with 22 arbitrary primers applied to 37 varieties produced 144 useful markers, of which 67% were polymorphic. Thus, with selected primers sufficient polymorphism could be detected to allow identification of individual varieties. Visual examination of electrophoresis gels and analysis of banding patterns confirmed that commercial Australian and USA lines and their relatives were very closely related, with similarity indices of 88-97%. Three varieties originating from more distant geographical centres were easily distinguished, producing variety-specific amplification profiles and expressing a lower **similarity index** of 80% to all other varieties tested. PCR offers a potentially simple, rapid and reliable method for rice genotype identification and recognition of lines that could contribute genetic diversity to new commercial varieties.

24/3,AB/20 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

08014293 Genuine Article#: 235YB Number of References: 32
Title: Low-Cot DNA sequences for fingerprinting analysis of germplasm diversify and relationships in Amaranthus (ABSTRACT AVAILABLE)
Author(s): Sun M (REPRINT) ; Chen H; Leung FC
Corporate Source: UNIV HONG KONG,DEPT ZOOL, POKFULAM RD/HONG KONG//HONG KONG/ (REPRINT)
Journal: THEORETICAL AND APPLIED GENETICS, 1999, V99, N3-4 (AUG), P464-472
ISSN: 0040-5752 Publication date: 19990800
Publisher: SPRINGER VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010
Language: English Document Type: ARTICLE
Abstract: We examined genetic diversity and relationships among 24 cultivated and wild Amaranthus accessions using the total low-Got DNA and five individual repetitive sequences as probes. These low-Cot DNA probes were obtained by the isolation of various classes of repetitive-DNA sequences, including satellites, minisatellites, microsatellites, rDNA, retrotransposon-like sequences, and other unidentified novel repetitive sequences. DNA fingerprints generated by different types of repetitive-DNA probes revealed different levels of polymorphism in the Amaranthus genomes. A repetitive sequence containing microsatellites was found to be a suitable probe for characterizing intraspecific accessions, whereas more conservative sequences (e.g. rDNA) were informative for resolving phylogenetic relationships among distantly related species. Genetic diversity, measured as restriction fragment length polymorphism (**RFLP**) and the **similarity index** at the low-Got DNA level, was equally high among intraspecific accessions between the two species groups: grain amaranths (A. caudatus, A. cruentus, and A. hypochondriacus) and their putative wild progenitors (A. hybridus, A, powellii, and A. quitensis). At the interspecific level, however, the grain amaranth species are less divergent from each other than their wild progenitors. With the rare exceptions of certain A. caudatus accessions, grain amaranths were found to be closely related to A. hybridus. The results based on low-Got DNA were comparable with previous **RAPD** and isozyme studies of the same set of species/accessions of Amaranthus, indicating that Tow-Got DNA sequences are suitable probes for a fingerprinting analysis of **plant** germplasm diversity and for determining phylogenetic relationships.

24/3,AB/21 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

06487072 Genuine Article#: YW662 Number of References: 29
Title: Identification and discrimination of eight Greek grape cultivars (Vitis vinifera L.) by random amplified polymorphic DNA markers (ABSTRACT AVAILABLE)
Author(s): Stavrakakis MN (REPRINT) ; Biniari K; Hatzopoulos P
Corporate Source: AGR UNIV ATHENS,LAB VITICULTURE, IERA ODOS 75/GR-11855 ATHENS//GREECE/ (REPRINT); AGR UNIV ATHENS,MOL BIOL LAB/GR-11855 ATHENS//GREECE/
Journal: VITIS, 1997, V36, N4 (DEC), P175-178
ISSN: 0042-7500 Publication date: 19971200
Publisher: BUNDESANSTALT ZUCHTUNGS FORSCHUNG KULTURPFLANZEN, INST REBENZUCHTUNG GEILWEILERHOF, D-76833 SIEBELDINGEN, GERMANY
Language: English Document Type: ARTICLE
Abstract: Fifteen decamer primers of an arbitrary nucleotide sequence were used to amplify genomic DNA by polymerase chain reaction (PCR- **RAPD**) in order to identify and discriminate between 8 cultivars of Vitis vinifera L., grown at the Island of Crete. Over 140 reproducible polymorphic fragments were generated by this method. Each grape **cultivar** showed a unique banding pattern for more than 5 of the primers used. Herefrom, the degree of genetic similarity was calculated and the dendrogram of the 8 cultivars was constructed. The results show that **RAPD** is a reliable and very useful method for the identification and genomic analysis of grape cultivars.

24/3,AB/22 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

06482313 Genuine Article#: YW571 Number of References: 39
Title: Assessment of genetic diversity of cultivated chickpea using microsatellite-derived RFLP **markers: Implications for origin** (ABSTRACT AVAILABLE)
Author(s): Serret MD (REPRINT) ; Udupa SM; Weigand F
Corporate Source: UNIV BARCELONA,FAC BIOL, UNITAT FISIOL VEGETAL, AVDA DIAGONAL 645/E-08028 BARCELONA//SPAIN/ (REPRINT); ICARDA,/ALEPPO//SYRIA/
Journal: PLANT BREEDING, 1997, V116, N6 (DEC), P573-578
ISSN: 0179-9541 Publication date: 19971200
Publisher: BLACKWELL WISSENSCHAFTS-VERLAG GMBH, KURFURSTENDAMM 57, D-10707 BERLIN, GERMANY
Language: English Document Type: ARTICLE
Abstract: Restriction fragment length polymorphism (**RFLP**) analysis was performed on 30 accessions of cultivated chickpea (Cicer arietinum L.) collected from 11 different countries representing the Near East, Central Asian and Hindustani regions. A synthetic digoxygenated oligonucleotide (GATA)(4) complementary to a microsatellite DNA sequence was used as a probe. The results revealed that simple repetitive sequences are abundant and polymorphic in the chickpea genome. The fragments detected were used to estimate the genetic diversity within accessions and a **similarity index** between the genotypes of the accessions. The genetic distance data were used to construct a dendrogram depicting genetic relationships among the different accessions. The results indicate that the greatest genetic diversity occurs in Pakistan, Iraq, Afghanistan, south-east Russia, Turkey and Lebanon. Lower genetic diversity was found in Iran, India, Syria, Jordan and Palestine. Based on DNA markers, it is concluded that there are three centres of diversity for chickpea: Pakistan-Afghanistan, Iraq-Turkey and Lebanon. India, which was previously considered as a secondary centre of diversity for chickpea, showed lower diversity than the above regions.

24/3,AB/23 (Item 4 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

04905483 Genuine Article#: UQ741 Number of References: 17
Title: DIVERSITY AMONG SOIL AND INSECT ISOLATES OF METARHIZIUM-ANISOPLIAE VAR ANISOPLIAE DETECTED BY RAPD (Abstract Available)
Author(s): FUNGARO MHP; VIEIRA MLC; PIZZIRANIKLEINER AA; DEAZEVEDO JL
Corporate Source: UNIV ESTADUAL LONDRINA,DEPT BIOL GERAL,CAIXA POSTAL 6001/BR-86051970 LONDRINA//BRAZIL/; UNIV SAO PAULO,ESCUELA SUPER AGR LUIZ DE QUEIROZ,DEPT GENET/PIRACICABA/SP/BRAZIL/
Journal: LETTERS IN APPLIED MICROBIOLOGY, 1996, V22, N6 (JUN), P389-392
ISSN: 0266-8254
Language: ENGLISH Document Type: ARTICLE
Abstract: Random amplified polymorphic DNA (**RAPD**) was used in order to analyse the relationships among 13 isolates of Metarhizium anisopliae var. anisopliae. Six of them were isolated from Deois flavopicta (Stal) (Hemiptera-Homoptera : Cercopidae) in different regions of Brazil. The other seven were isolated from soil in Parana State in Southern Brazil. The isolates were grouped by cluster analysis using Dice **similarity index** . The results show that isolates of M. anisopliae var. anisopliae are extremely diverse (47% similarity) but those isolated from D. flavopicta present only a moderate degree of variation (82% similarity) when compared with the wide diversity (31% similarity) found in the group isolated from soil. These results suggest that M. anisopliae var. anisopliae has developed host specificity.

24/3,AB/24 (Item 1 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01562539 2000223508
A study of genetic variation and relationships within the bamboo subtribe Bambusinae using amplified fragment length polymorphism
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EMAIL: yygan@nie.edu.sg
Journal: Annals of Botany, 85/5 (607-612), 2000, United Kingdom
CODEN: ANBOA
ISSN: 0305-7364
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 20

Taxonomic and systematic studies of the woody bamboos are traditionally based on floral morphology, which can cause problems in identification due to the lack of, or infrequent, flowering. Limited studies have been conducted using molecular techniques to overcome this problem. In this study, we used amplified fragment length polymorphisms (AFLPs) to conduct a study of four genera of bamboos (Bambusa, Dendrocalamus, Gigantochloa and Thyrsostachys) in the subtribe Bambusinae. **AFLP** analysis using eight primer combinations was carried out on 15 species of bamboo. Results showed that AFLPs distinguish the different species by their unique banding patterns. Unique AFLPs were detected in 13 of the 15 species examined. The six Bambusa species examined separated into two clusters. The six Gigantochloa species studied formed a discrete cluster diverging from one of the Bambusa clusters, while Thyrsostachys was less similar to the Bambusa clusters. The **similarity index** between B. lako and G. atroviolacea was the highest, suggesting that B. lako is more appropriatety included within the genus Gigantochloa rather than the genus Bambusa. The two Dendrocalamus species examined were very different with D. brandisii clustering within one of the Bambusa clusters and D. giganteus appearing as a very distant species. These results support the contention that critical study of the genus Dendrocalamus is required. The use of AFLPs for identification of particular bamboo species, as well as for the study of relationships within the subtribe, will be useful for industrial purposes and for systematic studies. (C) 2000 Annals of Botany Company.

24/3,AB/25 (Item 2 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01450002 2000125833
Genetic diversity and relationships of sweetpotato and its wild relatives in Ipomoea series Batatas (Convolvulaceae) as revealed by inter-simple sequence repeat (ISSR) and restriction analysis of chloroplast DNA
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EMAIL: meisun@hkucc.hku.hk
Journal: Theoretical and Applied Genetics, 100/7 (1050-1060), 2000, Germany
CODEN: THAGA
ISSN: 0040-5752
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 36

Genetic diversity and relationships of 40 accessions of Ipomoea, representing ten species of series Batatas, were examined using ISSR markers and restriction-site variation in four non-coding regions of chloroplast DNA. A total of 2071 ISSR fragments were generated with 15 primers in these accessions and, on average, 52 bands per accession were amplified. Most of the primers contained dinucleotide repeats. The ISSR fragments were highly polymorphic (62.2%) among the 40 accessions studied. Restriction analysis of chloroplast (cp) DNA revealed 47 informative restriction-site and length mutations. Phylogenetic analyses of ISSR and cpDNA datasets generally revealed similar relationships at the interspecific level, but the high polymorphism of ISSRs resulted in a better separation of intraspecific accessions. However, the combined ISSR and cpDNA dataset appeared to be appropriate in resolving both intra-and interspecific relationships. Of the species examined, I. trifida was found to be the most closely related to cultivated sweetpotato, the hexaploid I. batatas, while I. ramosissima and I. umbraticola were the most distantly related to I. batatas within the series. Ipomoea triloba, hitherto considered to be one of the ancestors of sweetpotato, was only distantly related to sweetpotato based on ISSR **similarity index** .

24/3,AB/26 (Item 3 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01193138 1999166299
Effects of repeated harvesting of forest residues on the ectomycorrhizal community in a Swedish spruce forest
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Journal: New Phytologist, 142/3 (577-585), 1999, United Kingdom
CODEN: NEPHA
ISSN: 0028-646X
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 44

for fossil fuels, which contribute substantially to the increase in [COinf 2] in the atmosphere. However, increased harvesting of forest residues for biofuel might affect the availability of base cations, P and N, as well as the development, community dynamics and function of ectomycorrhizas. This in turn might influence nutrient uptake and tree growth. In this study we investigated the effects of repeated forest residue harvesting on ectomycorrhizal species colonizing spruce roots in the humus layer of a 35-yr-old forest. Harvesting significantly decreased the thickness of the humus layer as well as decreasing the numbers of ectomycorrhizal root tips

both per metre root length and per unit humus volume. Changes in mycorrhizal community structure were studied by ITS typing with the use of PCR- **RFLP** analysis. In total, 19 different ITS types were found on two different sampling occasions (autumn and spring); 11 of these were common to both samplings. Nine of the ITS types were identified to at least the genus level by comparison with **RFLP** patterns of identified fruiting bodies or axenic cultures. Five species, Cortinarius sp. 2, Thelephora terrestris (Ehrenb.) Fr., Lactarius theiogalus (Bull.:Fr.) S. F. Gray s.st. Neuhoff, Tylospora fibrillosa Donk and To-96-12, occurred on over 5% of the total sampled root tips. Together these five types colonized 63% of the mycorrhizas screened. A **similarity index** assessment showed no shift in mycorrhizal community structure as a result of harvesting. Our findings suggest that the repeated removal of forest residues might have a strong effect on the quantity and development of ectomycorrhizal roots in the organic horizon, but little effect on the species composition of the community.

24/3,AB/27 (Item 4 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01184952 1999159554
Potential of DNA markers in detecting divergence and in analysing heterosis in Indian elite chickpea cultivars
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Journal: Theoretical and Applied Genetics, 98/8 (1217-1225), 1999, Germany
CODEN: THAGA
ISSN: 0040-5752
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 38

Molecular markers such as RAPDs and microsatellites were used to study genetic diversity in 29 elite Indian chickpea genotypes. In general, microsatellites were more efficient than the **RAPD** markers in detecting polymorphism in these genotypes. Among the various microsatellites, (AAC)$D5, (ACT)$D5, (AAG)$D5 and (GATA)inf 4 were able to differentiate all 29 chickpea cultivars. The mean value of probability of identical match by chance was 2.32 x 10sup -sup 2sup 5 using DraI-(ACT)$D5, TaqI-(AAC)$D5, TaqI-(AAG)$D5 and TaqI-(GATA)inf 4 enzyme-probe combinations. The dendrogram, constructed on the basis of **similarity index** values, grouped the chickpea genotypes into five main clusters with 8 cultivars genetically distant and outgrouped from the main clusters. To investigate if DNA markers are useful in predicting Finf 1 performance and heterosis in chickpea, we crossed 8 genotypes having important agronomic characters in a diallel set. The Finf 1s and their parents in the diallel set were analysed for agronomic traits for better parent and midparent heterosis. Heterosis was found to be much higher for yield than for yield components that fit a multiplicative model. The analysis of genetic divergence using Dsup 2 statistics clustered the 8 cultivars into two groups. Although molecular marker-based genetic distance did not linearly correlate to heterosis, two heterotic groups could be identified on the basis of the general marker heterozygosity.

24/3,AB/28 (Item 5 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

00995055 1998241528
Molecular phylogeny of mangroves V. Analysis of genome relationships in mangrove species using RAPD and RFLP markers
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Journal: Theoretical and Applied Genetics, 97/4 (617-625), 1998, Germany
CODEN: THAGA
ISSN: 0040-5752
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 43

DNA from pooled leaf samples of 11 true major mangrove, three true minor mangrove, two mangrove associate, two mangrove parasite, three terrestrial and one cultivated species were isolated for the present study. In total, 198 random amplified polymorphic DNAs (RAPDs) and 180 restriction fragment length polymorphism (**RFLP**) loci were scored by using ten primers and 14 enzyme-probe combinations respectively. The polymorphism observed for these markers revealed a high degree of genetic diversity in mangroves at both inter-specific or inter-generic levels. A dendrogram, constructed after pooling both **RAPD** and **RFLP** data, using a **similarity index** was analysed for genome relationships among these species. The dendrogram showed clustering of all the major mangroves, except for Nypa fruticans (Arecaceae), into one group. All species under the tribe Rhizophorae formed a subcluster, to which Xylocarpus granatum was found to be the most closesly related species. The clustering pattern implied that Excoecaria agallocha and Acanthus ilicifolius should be considered as true minor mangroves. The present study also provided molecular data favouring the separation of Avicennia spp. from the Verbenaceae to create a monotypic family the Avicenniaceae. The separation of Viscum orientale into the Viscaceae was also favoured.

24/3,AB/29 (Item 6 from file: 71)

00990172 1998238529
Genetic study of grape cultivars belonging to the muscat family by random amplified polymorphic DNA markers
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Journal: Vitis, 37/3 (119-122), 1998, Germany
CODEN: VITIA
ISSN: 0042-7500
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 17

Eleven decamer primers of arbitrary nucleotide sequence were used to amplify genomic DNA through the polymerase chain reaction (PCR- **RAPD**) in order to identify and discriminate between 14 grape cultivars (types or synonyms) belonging to the muscat family. Over 115 reproducible polymorphic fragments were generated by this method. On the basis of these fragments the degree of genetic similarity was calculated and the dendrogram of the 14 cultivars was established. The results indicate that there is genetic variation among the cultivars of the muscat family with values of the genetic similarity ranging from 0.666 to 1.00. On the basis of the observed bands it was possible to identify and discriminate between the cultivars studied except for Moschato aspro and Moscudi which were found to be identical.

24/3,AB/30 (Item 7 from file: 71)

00768079 1998014933
Isozyme and RAPD **analysis of the genetic diversity within and between Vigna luteola and V. marina**

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Journal: Annals of Botany, 80/6 (741-746), 1997, United Kingdom
PUBLICATION DATE: 19970000
CODEN: ANBOA
ISSN: 0305-7364
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 30

Nineteen accessions of Vigna luteola, five of V. marina ssp. oblonga, and two of V. marina ssp. marina were analysed using variation of isozymes and **RAPD** markers to obtain better insight into genetic relationships within and between these taxonomic entities. Thirteen putative isozyme loci were scored, seven of which were polymorphic. Both species showed very low genetic diversity indices and most of the variation was detected among populations. Pairwise Nei's genetic distances based on allozyme frequencies were also very low and the accessions of V. marina ssp. marina were the least related to the others. **RAPD** analysis was more discriminating and 66 bands out of a total of 85 were polymorphic. Based on the presence or absence of bands, Jaccard's **similarity index** was calculated. Similarity ranged from 0.476 to 0.98. Matrices derived from both isozyme and **RAPD** data were used to construct UPGMA dendrograms. In the tree obtained from Nei's genetic distance, based on allozyme frequencies, accessions belonging to V. marina ssp. oblonga were mixed with V. luteola accessions; on the other hand, the two V. marina ssp. marina clustered separately, with one V. luteola. The dendrogram derived from **RAPD** data showed three main groups corresponding to the three taxa analysed. Moreover, according to these data, V. marina ssp. oblonga is more closely related to V. luteola than to V. marina ssp. marina.

24/3,AB/31 (Item 8 from file: 71)

00765489 1997274024
Genetic characterisation of oak seedlings, epicormic, crown and micropropagated shoots from mature trees by RAPD **and microsatellite PCR**
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Journal: Scientia Horticulturae, 70/4 (319-330), 1997, Netherlands
PUBLICATION DATE: 19970000
CODEN: SHRTA
ISSN: 0304-4238
PUBLISHER ITEM IDENTIFIER: S0304423897000654
DOCUMENT TYPE: Article
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 32

DNA was isolated from seedlings of Quercus, robur, collected from a single provenance, and from epicormic, crown shoots and in vitro shoots from a single tree of Q. petraea using a CTAB method of extraction. DNA was obtained in sufficient quantity and purity, from 13 out of 30 seedlings, and from all isolations from epicormic and in vitro shoots (2.5-10.0 mug/g fresh/weight). Smearing was minimised at a primer concentration of 0.12 muM with Taq polymerase at 0.5 unit/reaction. Nine primers produced 142 bands 28 of which were polymorphic. A **similarity index** showed that 11 seedlings were closely related with high coefficients (0.85-0.90), but each could be identified from another using only 9 primers (OPA-02 and -05, OPG-04 and -05, OPE-01, -02, -03, -08, -09). DNA was isolated from crown, epicormic and in vitro leaves originating from a single 150-yr old tree of Q. petraea and analysed by randomly amplified polymorphic DNA (**RAPD**) and microsatellites. With each primer, a characteristic **RAPD** pattern was obtained, and it was common to all six epicormic shoots derived from different pans of a single branch of this tree; also to the shoots from the

crown of the same true with OPEl OPA-05, OPA-08, OPA-01, OPA-02, OPA-04, OPA-05, OPG-02, OPG-10, OPE-12. Similarly, the **RAPD** pattern obtained from shoot cultures in vitro, derived from individual nodes of epicormic shoots produced by six different branch segments were uniform for each of 15 primers. This work was repeated using microsatellite PCR. Three microsatellite loci AG16 AG 1/2 and AG 1/5 were amplified by PCR. It showed a uniformity of these microsatellite loci in shoots from the crown of the tree, and from epicormic shoots culture derived from six different sections of branch.

24/3,AB/32 (Item 1 from file: 73)
DIALOG(R)File 73:EMBASE

05127503 EMBASE No: 1992267719
Molecular phylogeny of the Helianthus genus, based on nuclear restriction- fragment-length polymorphism (RFLP)
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Genetique Moleculaire Vegetale, Universite Blaise-Pascal Clermont II, 4 rue Ledru,F-63038 Clermont-Ferrand Cedex 1 France
Molecular Biology and Evolution (MOL. BIOL. EVOL.) (United States) 1992, 9/5 (872-892)
CODEN: MBEVE ISSN: 0737-4038
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The systematics of 44 species of the Helianthus genus were studied by digestion of total DNAs by three six-base restriction endonucleases (BgIII, EcoRV, and HindIII) and by probing with 10 nuclear probes, resulting in a mean number of 63 hybridization signals per sample. First, the number of substitutions, per nucleotide site, between each of the genomes was estimated on the basis of the distribution of 345 fragments between samples, according to the 'fragment method' of Nei and Li. These pairwise distances were used to construct evolutionary trees by means of the unweighted pair grouping with arithmetic means and by the neighbor-joining method. The phylogenics produced by these two methods, where all the sections and series defined by morphological classification are separated, mirror the botanical classification of the genus. However, the integration of polyploid species (2n = 4x or 2n = 6x) leads to their artificial separation from the diploids. The separation of H. petiolaris and H. neglectus from the Helianthus section could provide evidence for two distinct lineages of annual species within the Helianthus genus. Second, varimax factor analysis, based on the F matrix, allows separation of species according to the **similarity index** and gives a plane representation that is close to the morphological classification given by the weighted pair grouping with arithmetic means. Third, the changes in the accuracy of distance estimates according to the number of probe-enzyme combinations used show that 30 combinations produce a general dispersion of <5% on both sides of the mean value. Model fitting to the decreasing dispersion indicates that 60 probe-enzyme combinations would ensure a dispersion of distance estimation of <1%, even in the case of distantly related species.

24/3,AB/33 (Item 1 from file: 98)
DIALOG(R)File 98:General Sci Abs/Full-Text

04273619 H.W. WILSON RECORD NUMBER: BGSA00023619
Evidence of sexuality in European rubus (Rosaceae) species based on AFLP **and allozyme analysis.**
Kollmann, Johannes
Steinger, Thomas; Roy, Barbara A
American Journal of Botany (Am J Bot) v. 87 no11 (Nov. 2000) p. 1592-8
SPECIAL FEATURES: bibl diag graph il tab ISSN: 0002-9122
LANGUAGE: English
COUNTRY OF PUBLICATION: United States
WORD COUNT: 6641

ABSTRACT: Reproduction of polyploid Rubus species is described as facultatively apomictic. Pollination is needed for seed set, but most seedlings are produced asexually by pseudogamy. Although sexual processes may occur, clonal diversity can be extremely low. We performed a pollination experiment to investigate the breeding system and used allozyme and **AFLP** markers to analyze genetic variation among and within seed families in R. armeniacus and R. bifrons. Pollination either with self or outcross pollen was necessary to trigger seed set. Outbreeding marginally increased the number and quality of seeds compared with selfing. The enzyme PGI revealed some genetic variation within seed families. Seven other enzyme systems were monomorphic. The more detailed **AFLP** analyses with five primer pairs detected the same rate of genetic variation (14-17% of seedlings were genetically distinct) and confirmed the allozyme results for the same individuals. No genetic variation was found between the seed families from within a species collected in widely separated populations, but clear species-specific differences were observed. The results support the view that polyploid Rubus species are pseudogamous apomicts with low genetic diversity among and within seed families. However, sexual reproduction occasionally occurs and contributes to the maintenance of genetic variation within natural populations. Reprinted by permission of the publisher.

24/3,AB/34 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

13680272 PASCAL No.: 98-0388772
Hybrid performance and genetic distance as revealed by the (GATA) SUB 4 microsatellite and RAPD **markers in pearl millet**
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Journal: Theoretical and Applied Genetics, 1998, 97 (1-2) 163-169
Language: English
Genetic diversity in five cytoplasmic male-sterile and seven restorer lines of pearl millet was determined by DNA fingerprinting using a (GATA) SUB 4 microsatellite and randomly amplified polymorphic DNAs (RAPDs). A total of 160 polymorphic loci were generated and, based on the polymorphism data, **similarity index** values ranged from 0.81 to 0.50. Cluster analysis was performed and relationships among these lines revealed that they were not in agreement with the available pedigree data. The per se performance of parents and hybrids was analyzed for days-to-50% flowering, **plant** height, productive tillers, ear length, ear width, 1000-grain weight and grain yield per plot. Path co-efficient analysis revealed that productive tillers, ear width and days-to-50% flowering had a relatively large positive effect. The correlation values were mostly not significant with respect to genetic distance, except for days-to-50% flowering, ear length and ear width. Our results have indicated that genetic-distance measures based on the (GATA) SUB 4 microsatellite and RAPDs may be useful for the grouping of parents, but not for predicting heterotic combinations, in pearl millet.

24/3,AB/35 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal

12211786 PASCAL No.: 95-0429583
Comparison of Vitis berlandieri x Vitis riparia rootstock cultivars by restriction fragment length polymorphism analysis
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Journal: Vitis, 1995, 34 (2) 109-112

Language: English

S u m m a r y : Patterns produced by **RFLP** analysis of genomic DNA extracted from nine Berlandieri infinity riparia rootstock cultivars were compared. Of the six grape DNA probes used, several combinations of three probes were sufficient to clearly distinguish all nine rootstocks. Calculation of a **similarity index** for each pair revealed that 420 A was notably distinct from the other members of the group (D=0.56 compared to an average similarity of 0.77 among all the hybrids), while the Teleki hybrids (SO 4, 5 C, 5 BB, 125 AA, Cosmo 2, Cosmo 10) were generally very similar to each other (average D=0.85). No differences were observed between 5 A and 5 BB, consistent with previous reports that at least some 5 A vines are identical to 5 BB.

24/3,AB/36 (Item 3 from file: 144)

12094840 PASCAL No.: 95-0321312

Randomly amplified polymorphic DNA analysis of Xylella fastidiosa pierce's disease and oak leaf scorch pathotypes

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Journal: Applied and environmental microbiology, 1995, 61 (5) 1688-1690
Language: English

Randomly amplified polymorphic DNA analysis was conducted with 14 primers to 17 strains of Xylella fastidiosa. There was a high degree of similarity among the seven Pierce's disease (PD) strains (S SUB x SUB y >0.93) and the seven oak leaf scorch (OLS) strains (S SUB x SUB y >0.96). However, the two groups were different, with a **similarity index** of 0.67, confirming the presence of a PD DNA cluster and suggesting the presence of a new OLS cluster. The control plum leaf scald strains (two strains) together with the periwinkle wilt strain had a much smaller **similarity index** (0.44) compared with the PD and OLS clusters